

protein-protein **BLAST**

Search

```
lpvvkignpkni kpgewvaal gaprgtronsvt agivsa kgrs ipnesytpriqtava inpg  
nsggplfnlkgqvvginsqiysrsggfmgisfaipidvamnvaeklntgkvqrgqlgvii  
qevsyglaqsfgldkasgaliakipgspaeraglaqgdivlsldggeirssgdlpvmvgai  
tpgkevslgvwrkgeeitikaklgnaaehtgassktdeapyteqqsgtfsvesagitlqth  
tdssgkhlvvrsvdaaeraglrhgdeilavrprq
```

seq
ID NO: 4
091388, 080Set subsequence From: To: Choose database Do CD-Search ☒Now: **BLAST!** or **Reset query** **Reset all**

Options for advanced blasting

Limit by entrez query or select from: Composition-based statistics ☒Choose filter ☒ Low complexity ☐ Mask for lookup table only ☐ Mask lower caseExpect Word Size Matrix Gap Costs

PSSM

Other advanced PHI pattern



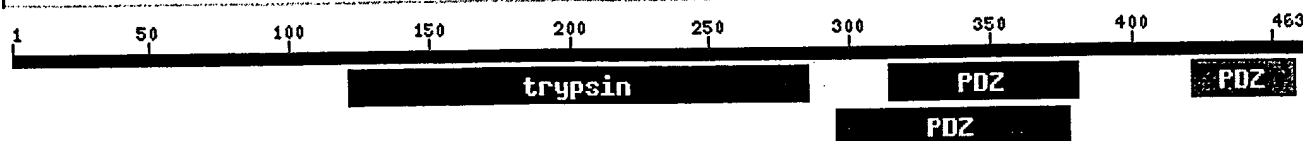
formatting BLAST

Your request has been successfully submitted and put into the Blast Queue.

Query = (463 letters)

Putative conserved domains have been detected

Click on the image below for detailed CD-Search results



The request ID is 1002310688-22263-27915

Format! or **Reset all!**

The results are estimated to be ready in 11 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ NCBI-gi Alignment in HTML format

Number of: Descriptions 100 Alignments 50

Alignment view Pairwise

Format for PSI-BLAST ☐ with inclusion threshold: 0.005

Limit results by entrez query or select from:

Expect value range:

NCBI

CD-Search

Entrez ?

RPS-BLAST 2.2.1 [Apr-13-2001]

Query=

(463 letters)

.. This CD alignment includes 3D structure. To display structure, download [Cn3D v3.00!](#)

Mouse-over boxes to display more information



PSSMs producing significant alignments:

		Score (bits)	E value
gnl Pfam pfam00089	trypsin, Trypsin. Proteins recognized include all proteins in ...	68.6	8e-13
gnl Smart smart00228	PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called D...	46.2	4e-06
gnl Smart smart00228	PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called D...	36.6	0.003
gnl Pfam pfam00595	PDZ, PDZ domain (Also known as DHR or GLGF).. PDZ domains are ...	40.4	2e-04

[gnl|Pfam|pfam00089](#), trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*).

query to multiple alignment, display sequences

CD-Length = 217 residues, 89.9% aligned
Score = 68.6 bits (166), Expect = 8e-13

```
Query: 121 GGLNFGSGFIISKNGYILTNTHTVVGMSIKVLL-----NDKREYTAKLIGSDVQS-- 171
Sbjct: 21  SSGHFCGSLISEN-WVLTAACHCVSGASSVRVVLGEHNLGTTEGTEQKFDVKKIIVHPNY 79

Query: 172 -----DVALLKIDATEEL-----PVVKIGNPKNLKPE--WVAAIGAPF--GFDNSVTAG 217
Sbjct: 80  NPDTNDIALLLKSPVTLGDTVRPICLPASSDLFVGTTCSVSGWGRTKNLGTSDTLQEV 139

Query: 218 IVSAKGRSLPNESYTP-----FIQTD----VAINPGNSGGPLFNLKGQVVGINSQIYSRS 268
Sbjct: 140 VVPIVSRETCSRAYSAGGTVTDTMICAGALGGKDACQGDSSGGLVCSDELGVIVSWGYGCA 199

Query: 269 GGFMGISFAIPIDVAMN 285
Sbjct: 200 VGN-YPGVYTRVSRULD 215
```

[gnl|Smart|smart00228](#), PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities.

query to multiple alignment, display

sequences

CD-Length = 86 residues, only 79.1% aligned
Score = 46.2 bits (108), Expect = 4e-06

```
Query: 314 QSFGLDKASGALIAKI-PGSPAERAGLQAGDIVLSLDGGEIRSSGDLPMVGAITPGKEV 372
Sbjct: 19  VGGKDSGDGGVVSVVPGSPAAGLKP GDVILEVNGTSVEGLTHLEAVDLLKEAGGKV 78

Query: 373 SLGVWRKG 380
Sbjct: 79  TLTVLRGG 86
```

- gnl|Smart|smart00228, PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities.

query to multiple alignment, display sequences

CD-Length = 86 residues, only 46.5% aligned
Score = 36.6 bits (83), Expect = 0.003

Query: 421 GITLQTHTDSSGKHLVVVRVSD--AAERAGLRHGDEILAV 458
Sbjct: 15 GFSLVGGKDSGDGGVVVSVVPGSPAAGLKPQDVILEV 54

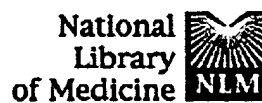
gnl|Pfam|pfam00595, PDZ, PDZ domain (Also known as DHR or GLGF).. PDZ domains are found in diverse signaling proteins.

query to multiple alignment, display sequences

CD-Length = 81 residues, 93.8% aligned
Score = 40.4 bits (93), Expect = 2e-04

Query: 295 KVQRGQLGVIIQEVSYGLAQSFGLDKASGALIAKI-PGSPAERAGLQAGDIVLSLDGGEI 353
Sbjct: 6 RQGRGGLGFSLKGGSDKGQ-----GIVVSEVLPGGAAERGGLKEGDRILEINGQDV 57

Query: 354 RSSGDLFVMVGAITPGKEVSLGVW 377
Sbjct: 58 ENVTHERAVLALKGSGGEVTLTVL 81



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